

FIG. 1

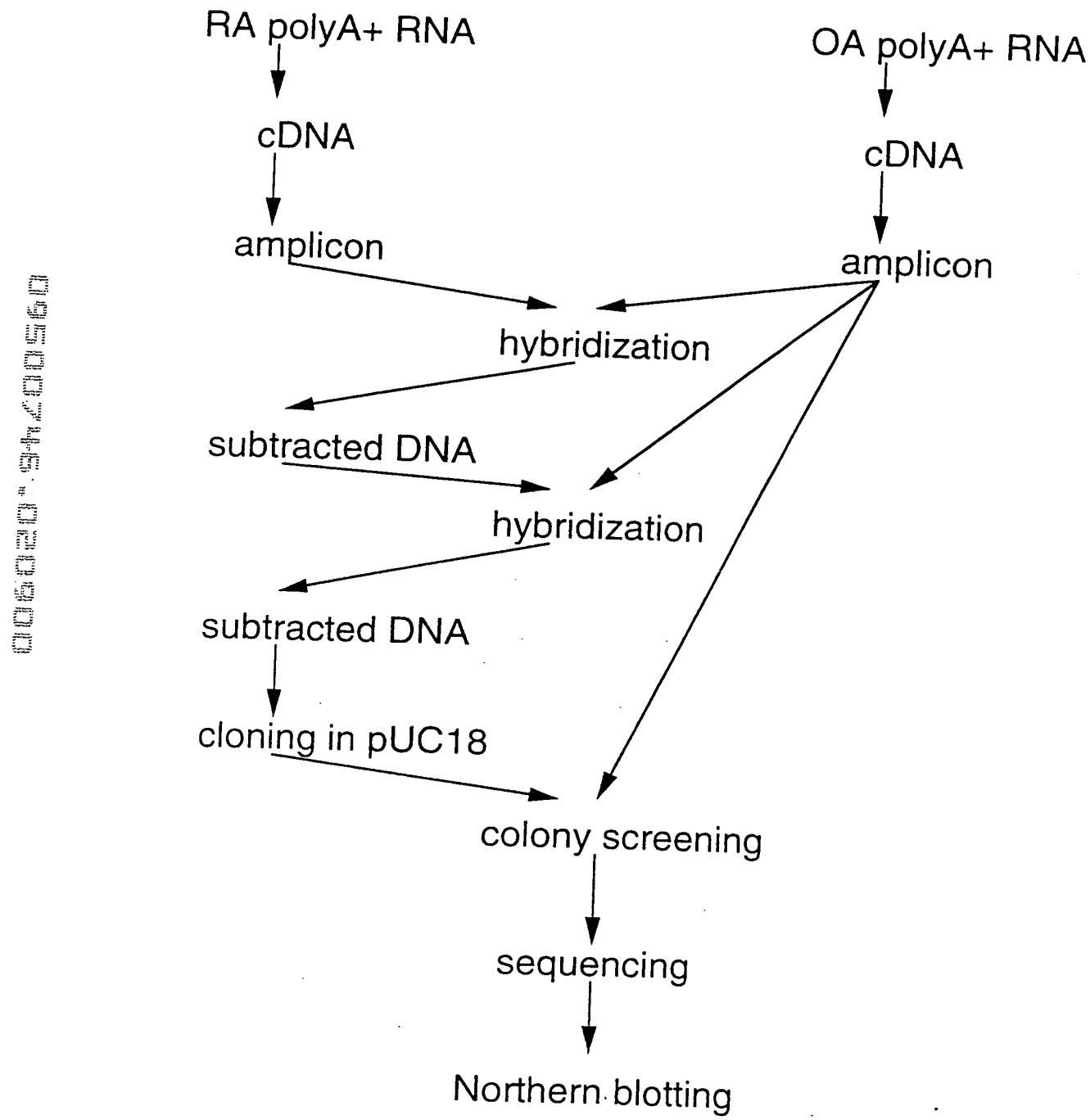


FIG. 2

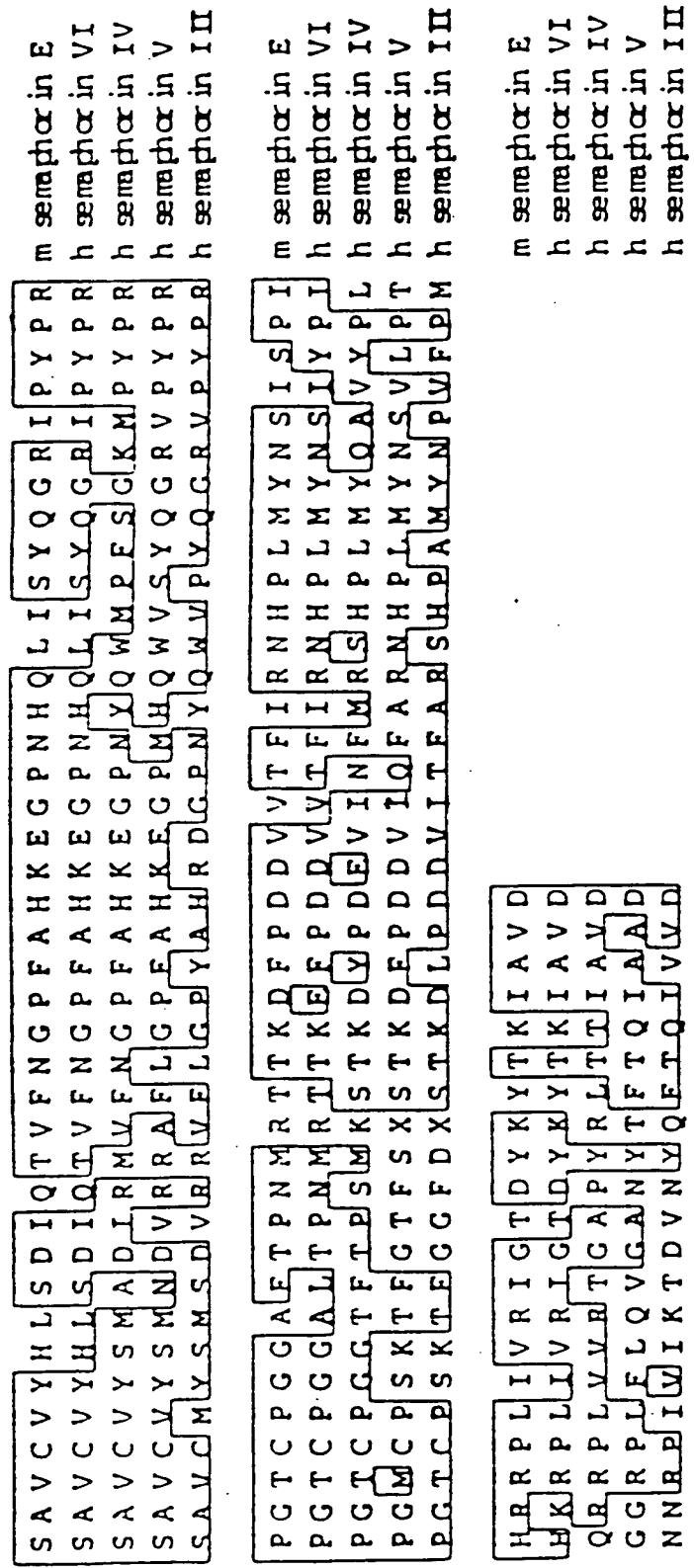


FIG. 3

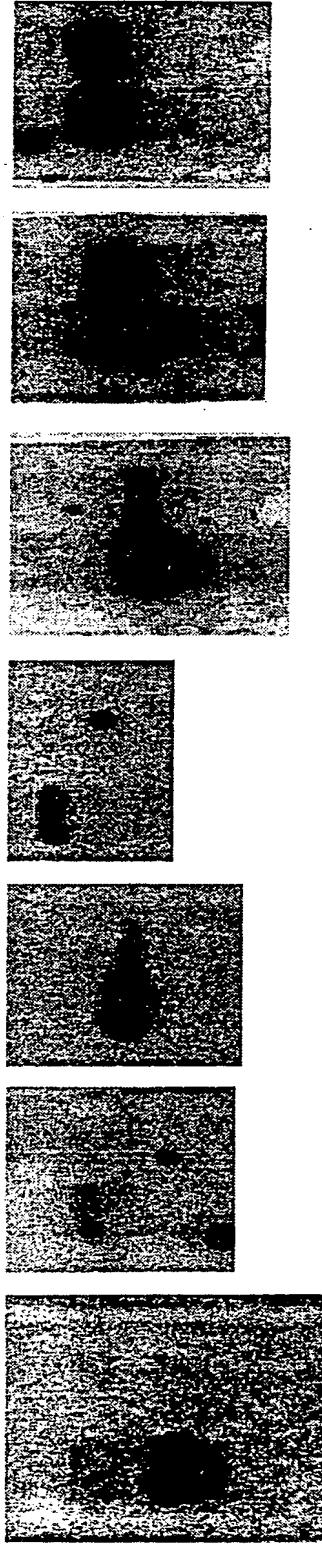
Y P A P H G P E D P A P Q F A H M F E N E I S H R T G S W N F A P N P D K Q W L L Q R T CELK09C4
S H A A P H G P E D S A P Q F S E L Y P N A S Q H I T P S Y N Y A P N M D K H W T M Q Y T ts99
A T P A P H S P W T A A P Q Y Q K A F Q N V F A P R N K N F N I H G T N K H W L I R Q A K GL6SHUMAN

G K M N D V H I S F T D L L H R R L Q T L Q S V D E G I E R L F N L L R E L N Q L W N T CELK09C4
G P M L P I H M E F T N I L Q R K R L Q T L M S V D D S V E R L Y N M L V E T G E L E N T ts99
T P M T N S S T Q F L D N A F R K R W Q T L L S V D D L V E K L V K R L E F T G E L N N T GL6SHUMAN

Y A I Y T S D H G Y H L G Q F G L L K G K N M P Y E F D I R V P F F M R G P G I P R CELK09C4
Y I I Y T A D H G Y H I G Q F G L V K G K S M P Y D F D I R V P F F I R G P S V E P ts99
Y I F Y T S D N G Y H T G Q F S L P I D K R Q L Y E F D I K V P L L V R G P G I K P GL6SHUMAN

FIG. 4

RA OA RA OA RA OA RA OA RA OA



ML2122 ML2115 lumican IGFBP5 SDF1a semVI collagenaseV

FIGURE 5

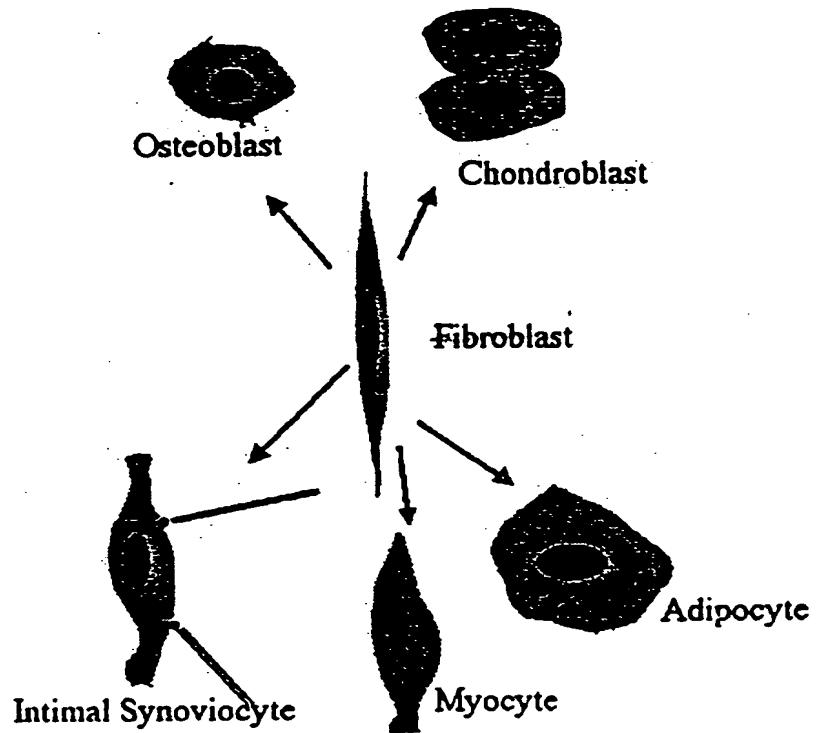
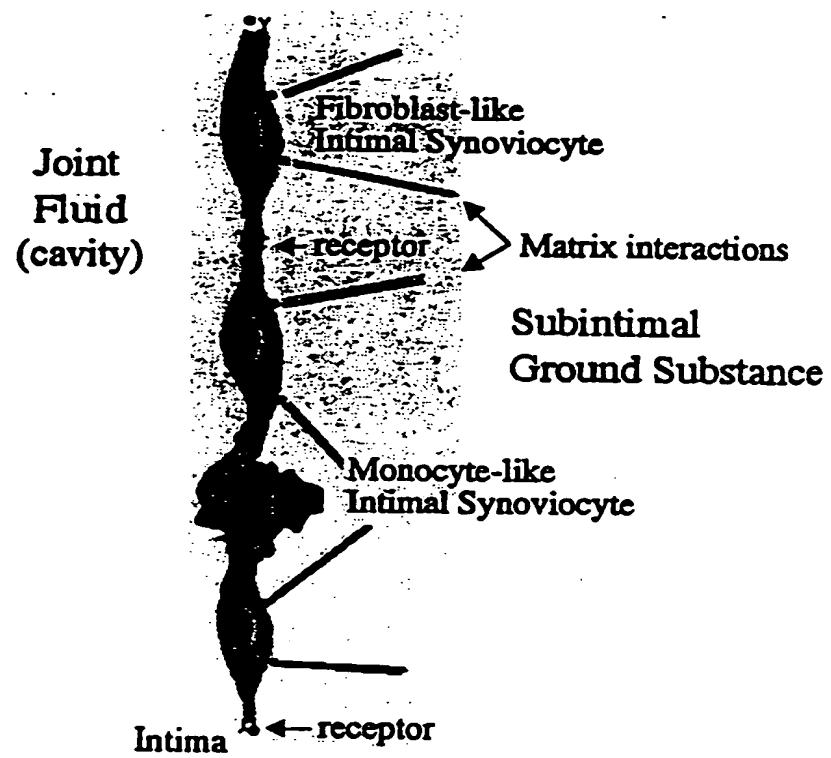


FIGURE 6



09250476-000000000000

FIGURE 7

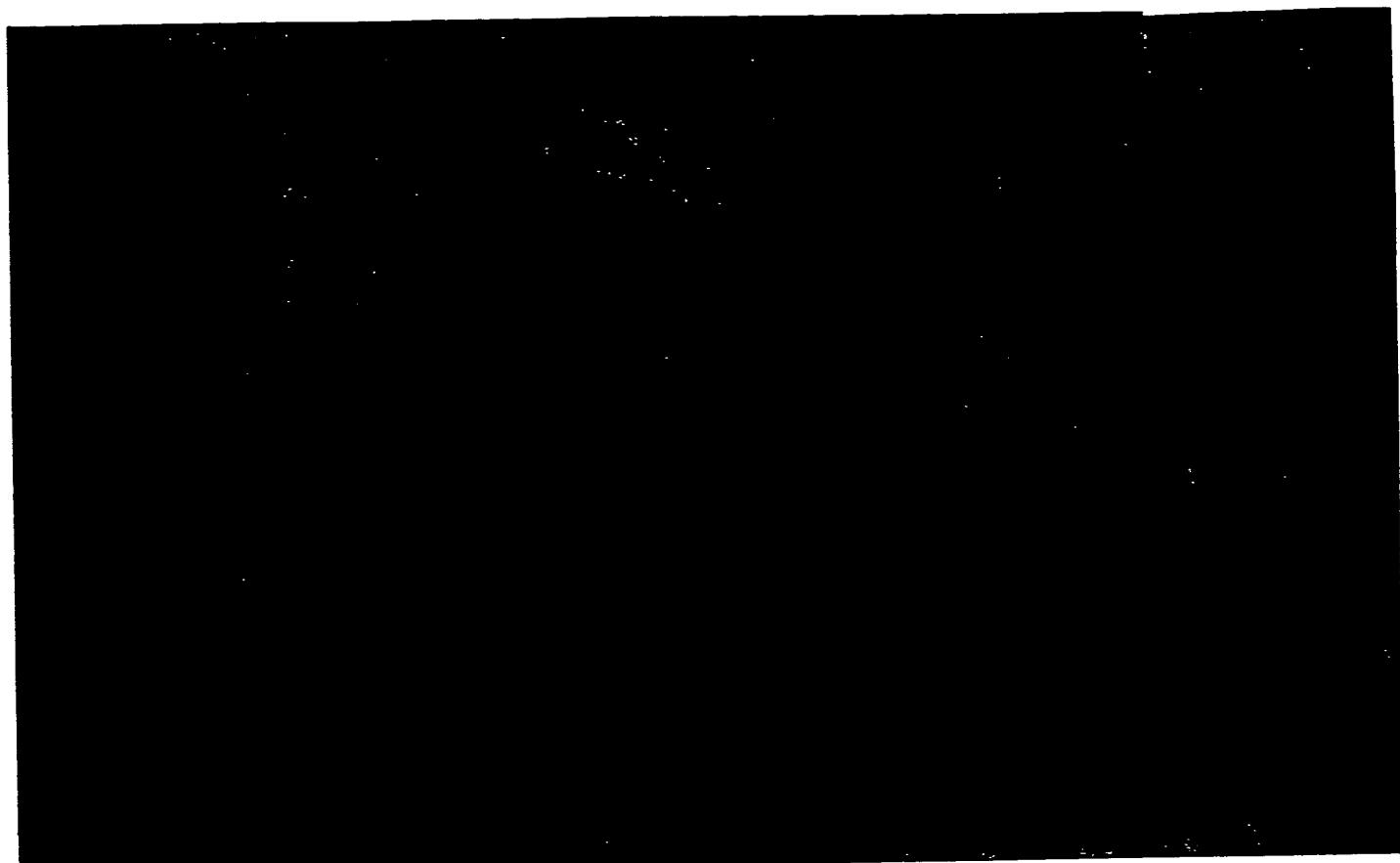


FIGURE 8

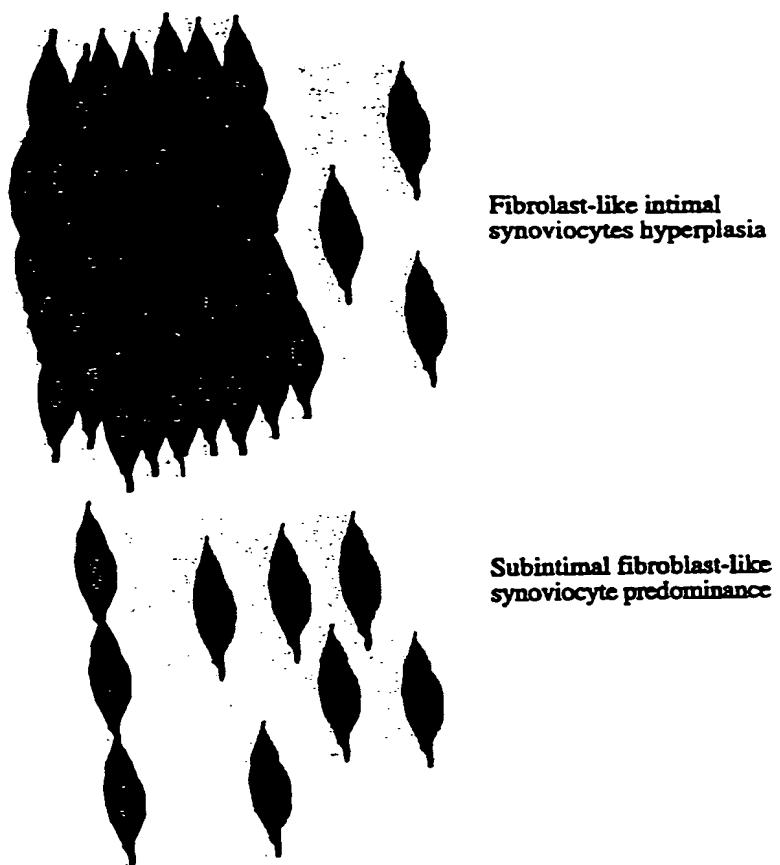


FIGURE 9

RA OA RA OA RA OA RA OA RA OA RA OA



ML2122 ML2115 lumican IGFBP5 SDF1a semVI collagenaseIV

FIGURE 10

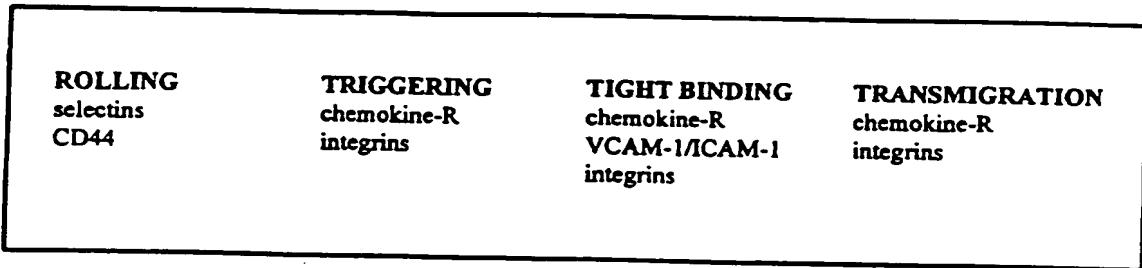
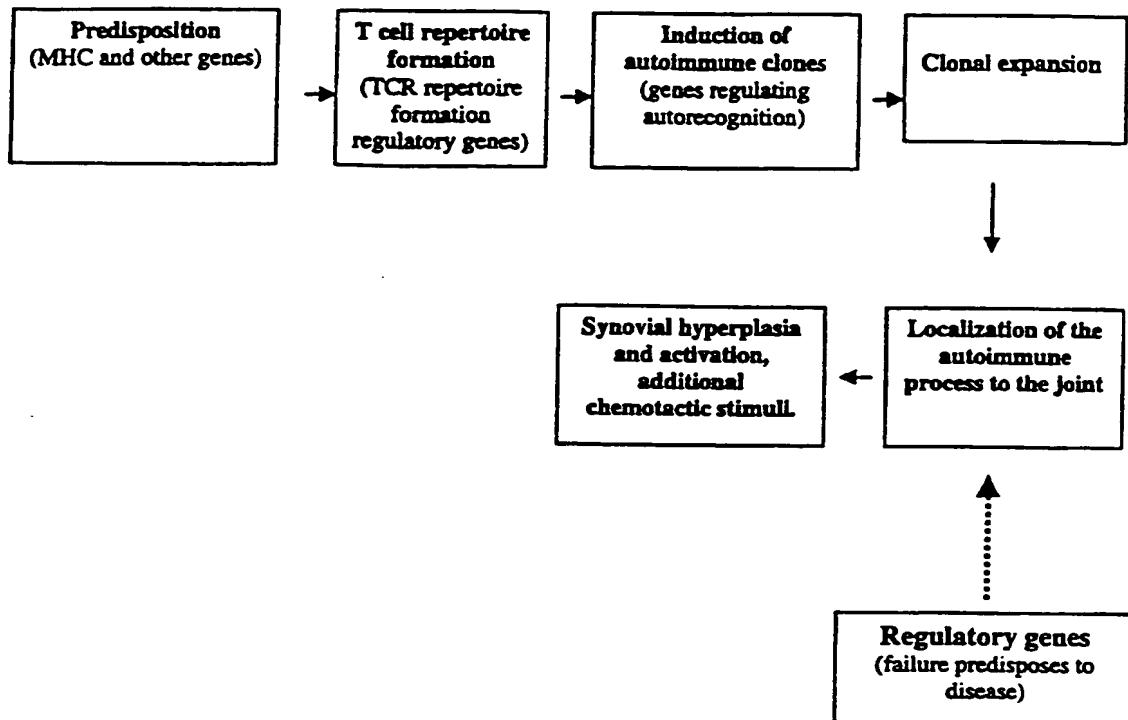


FIGURE 11



09500746 020908

FIGURE 12

10 20 30 40 50 60

New 95-04-12- 25.Seq(1>484) <- GNNGAGTGTGGGACGGGGGNGNAGNAATTAAAGGTAGNG-ATGGAGNANGGGTGCNTNG
 New 95-04-12- 27.Seq(1>437) >- CCCGGGTACCGAGCTCGAATTCCGTTG
 GXXGAGTGTGGGACGGGGGXAGXAATTAAAGSYMGGGtAYSGAGCWGRRKTSCTGTTG

70 80 90 100 110 120

New 95-04-12- 25.Seq(1>484) <- GNNNAGANANTGNNTGGAGAANGACAANGGGGGNTCGNNGGAGGNNTGTGA-GTGGG
 New 95-04-12- 27.Seq(1>437) >- NTGTCGCCCTTGN-TGTG-----CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTG
 New 95-04-12- 01.Seq(1>382) >- CAGATGCCCATGCCGATTCTTCGAAAGCCATGTTG
 New 95-03-30- 34.Seq(1>439) >- CAGATGNCCATGCCGATTCTTCGAAAGCCATGTTG
 New 95-04-12- 21.Seq(1>466) <- CCATGTTGC
 GTGTMGMCRTTGxxTGKMGaaxgaCAGATGSCCATGCCGATTCTTCGAAAGCCATGTTG

130 140 150 160 170 180

New 95-04-12- 25.Seq(1>484) <- AAGAAGGCACGTCAANAAGGACGAATATTGCAANGNNNCAGGGCTGTNCNGGGCA
 New 95-04-12- 27.Seq(1>437) >- CAGA-GCCAACGTCAAGCATCTAAA-ATTCTAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-04-12- 01.Seq(1>382) >- CAGA-GCCAACGTCAAGCATCTAAA-ATTCTAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-03-30- 34.Seq(1>439) >- CAGA-GCCAACGTCAAGCATCTAAA-ATTCTAACACTCC-AAA--CTGTGCCCTT-CA
 New 95-04-12- 21.Seq(1>466) <- AAGA-NCCA-CGTCAA-CATCCAAA-AT-CTCAACACNCC-CAA--CTNTTCCCTT-CA
 MAGA-GCCAACGTCAAGCATCHCAA-ATTCTAACACTCC-MAA--CTGTGCCCTT-CA

190 200 210 220 230 240

New 95-04-12- 25.Seq(1>484) <- GTTGTGAAAAAAAAAAAAGAACNGCAGACAGACAAGTGTNNG-TTGACCCGAAGC-NA
 New 95-04-12- 27.Seq(1>437) >- GATTGTAGCCCGGCTGAAGAACAAAC-A--GACAAGTGTGCA-TTGACCCGAAGCTAA
 New 95-04-12- 01.Seq(1>382) >- GATTGTAGCCCGGCTGAAGAACAAAC-A--GACAAGTGTGCA-TTGACCCGAAGCT-A
 New 95-03-30- 34.Seq(1>439) >- GATTGTAGCCCGGCTGAAGAACAAAC-A--GACAAGTGTGCA-TTGACCCGAAGCT-A
 New 95-04-12- 21.Seq(1>466) <- GATTGTAGCCCGGCTGAAGAACAAAC-A-AGACAAGTGTGCAATTGACCGAAGCTAA
 GATTGTAGCCCGGCTGAAGAACAAAC-A-aGACAAGTGTGCA-TTGACCCGAAGCTAA

250 260 270 280 290 300

New 95-04-12- 25.Seq(1>484) <- NAGTGGATNCAGGAGTACC-TGGAGNNAA-CTATGAACAANTAAAGCGAACAGCC-AAAG
 New 95-04-12- 27.Seq(1>437) >- A-GTGGATTTCAGGAGTACC-TGGAG-AAAGCTTAAACAAGTAAGCACAACAGCC-AAAA
 New 95-04-12- 01.Seq(1>382) >- AAGTGGATTTCAGGAGTACC-TGGAGGAAAGCTTAAACAAGTAAGCACAACAG-CCAAAA
 New 95-03-30- 34.Seq(1>439) >- AAGTGGATTTCAGGAGTACC-TGGAGTAAAGCTTAAACAAGTAAGCACAACAG-NCAAAA
 New 95-04-12- 21.Seq(1>466) <- AAGTGGATTTCAGGAGTACC-TGGAG-AAAGCTTAAACAAGTAAGCACAACAGCCCCAAA
 AAGTGGATTTCAGGAGTACC-TGGAG-AAAGCTTAAACAAGTAAGCACAACAGCcAAAA

310 320 330 340 350 360

New 95-04-12- 25.Seq(1>484) <- AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGNCAA
 New 95-04-12- 27.Seq(1>437) >- AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGGCAA
 New 95-04-12- 01.Seq(1>382) >- AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGGCAA
 New 95-03-30- 34.Seq(1>439) >- AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGGCAN
 New 95-04-12- 21.Seq(1>466) <- AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGNCAA
 New 95-04-12- 19.Seq(1>463) <- AN-TGAAGGGCCAA

AGGACTTCCGCTAGACCCACTCGAGGAAACTAAACCTTGTGAGAGATGAAAGGSCAA

370 380 390 400 410 420

New 95-04-12- 25.Seq(1>484) <- AGACGTGGGGG-AGGGGGCCTAAC-CA-TGAGGACCAGGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 27.Seq(1>437) >- AGACGTGGGGGAGGGGGCTTAAC-CA-TGAGGACCAGGTGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 01.Seq(1>382) >- NGACGTNGNGG-AGGGGGCTTAACC-AT-GAGGACCAGGTGTGTGTGTGGGG-TGGG-C
 New 95-03-30- 34.Seq(1>439) >- TGTNTTGTGG-AGGGGGCTTAACC-AT-GAGGACCAGGTGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 21.Seq(1>466) <- AGACGTGGGGG-AGGGGGCTTAAC-CA-TGAGGACCAGGTGTGTGTGGGG-TGGG-C
 New 95-04-12- 19.Seq(1>463) <- AGACGTGGGGG-AGGGGGCTTAACCCATTGAGGACCAGNTGTGTGTGGGGGTGGC-C
 WGACGTGKGG-AGGGGGCTTAACccAttGAGGACCAGGTGTGTGTGGGGgTGGG-C

430 440 450 460 470 480

New 95-04-12- 25.Seq(1>484) <- ACATTG-ATCT-GGG-ATCGGGCCTGAGGTTGCCAGCATTAGACCCCTGCATTATAGC
 New 95-04-12- 27.Seq(1>437) >- ACATTGGATCTTN-G-ATCGGGCCTGAGGTTGCCAGCATTAGACCCCTGGATTAT-GN
 New 95-04-12- 01.Seq(1>382) >- ACATTGNATCTGGG-ATCGGGCCTGAGGTTGCCAGAATTNGNCCTGNATTNTGGN
 New 95-03-30- 34.Seq(1>439) >- ACATNGNATCT-GGGTATCGGGCCTGAGGTTGNCAGCATTAGNCCTGNATTATNGC
 ACATTGxATCTtGGG-ATCGGGCCTGAGGTTGSCAGCATTAGACCCCTGSATTATRGC

430 440 450 460 470 480
 New 95-04-12- 21.Seq(1>466) <- ACATTG-ATCT-GGG-ATCGGGCCTGAGGTTGCCAGCATTTAGACCCCTGCATTATAGC
 New 95-04-12- 19.Seq(1>463) <- ACATTG-ATCT-GGG-ATCGGGCCTGAGGTTGCCAGCATTTAGACCCCTGCATTATAGC
 ACATTGxATCTtGGG-ATCGGGCCTGAGGTTGCCAGCATTTAGACCCCTGSATTATAGC
 490 500 510 520 530 540
 New 95-04-12- 25.Seq(1>484) <- ATACGGTATGATATTGCAG
 New 95-04-12- 27.Seq(1>437) -> ATACGGNNTGATNTNN
 New 95-04-12- 01.Seq(1>382) -> ATCC
 New 95-03-30- 34.Seq(1>439) -> ATACGGCATGATATTGCAGNTTAT-TTCATCCATGCCNCGTACCTGTGNACGTTGGGAC
 New 95-04-12- 21.Seq(1>466) <- ATACGGTATGATATTGCAGCTTATTCATCCATGCC-TGTACCTGTGCACGTTGGAAC
 New 95-04-12- 19.Seq(1>463) <- ATACGGTATGATATTGCAGCTTATTCATCCATGCC-TGTACCTGTGCACGTTGGAAC
 ATACGGYATGATATTGCAGCTTATTCATCCATGCCxYGTACCTGTGCACGTTGGRAC
 550 560 570 580 590 600
 New 95-03-30- 34.Seq(1>439) -> TAG
 New 95-04-12- 21.Seq(1>466) <- TTTTATTACTGGGGTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTC-GACA
 New 95-04-12- 19.Seq(1>463) <- TTTTATTACTGGGGTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTCaAG-CAG
 TWKTATTACTGGGGTTTTCTAAGAAAGAAATTGTATTATCAACAGCATTTCaGaCAG
 610 620 630 640 650 660
 New 95-04-12- 19.Seq(1>463) <- TTAGTTCCCTCATGATCATACAATCATCATCATTCTCATTTCATTAAATC-AAC
 New 95-04-12- 17.Seq(1>461) <- GGTCACTNCATACTCATCATCATTCTCATTTCATTAAATCCAAAC
 TTAGTTCCCTCATGRTCACTACAATCATCATCATTCTCATTTCATTAAATC^cAAAC
 670 680 690 700 710 720
 New 95-04-12- 19.Seq(1>463) <- GAGTACTTCAGATCTGAATTGGCTTGTGGAGCATCTCCTCTGCTCCCTGGGGAGT
 New 95-04-12- 17.Seq(1>461) <- GAGTACNTCAAGATCTG-ATTGGCTTGTGGAGCATCTCCTCTGCTCCCTGGGGAGT
 GAGTACTTCAGATCTG^aATTGGCTTGTGGAGCATCTCCTCTGCTCCCTGGGGAGT
 730 740 750 760 770 780
 New 95-04-12- 19.Seq(1>463) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGTCCCTTCTCAGACA
 New 95-04-12- 17.Seq(1>461) <- CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGTCCCTTCTCAGACA
 New 95-03-30- 09.Seq(1>445) -> GGGAGCTGGAAAAAGTGTCCCTTCTCAGACA
 CTGGGCACAGTCAGGTGGTGGCTTAACAGGGAGCTGGAAAAAGTGTCCCTTCTCAGACA
 790 800 810 820 830 840
 New 95-04-12- 19.Seq(1>463) <- CTGAGGCTCCCGCAGCAGCGCCCTCCAAAGAGGAAGG
 New 95-04-12- 17.Seq(1>461) <- CTGAGGCTCCCGCAGCAGCGCCCTCCAAAGAGGAAGGCCTCTGTGGCACTCAGATAACCG
 New 95-03-30- 09.Seq(1>445) -> CTGAGGCTCCCGCAGCAGCGCCCTCCAAAGAGGAAGGCCTCTGTGGCACTCAGATAACCG
 CTGAGGCTCCCGCAGCAGCGCCCTCCAAAGAGGAAGGCCTCTGTGGCACTCAGATAACCG
 850 860 870 880 890 900
 New 95-04-12- 17.Seq(1>461) <- ACTGGGGCTGGGCGCCACTGCCTTCACCTCCCTTTCAACCTCAGTGATTGGCTCTG
 New 95-03-30- 09.Seq(1>445) -> ACTGGGGNTGGGCGCCACTGNCTTCACCTCCCTTTCAACCTCAGTGATTGGCTCTG
 ACTGGGGCTGGGCGCCACTGCCTTCACCTCCCTTTCAACCTCAGTGATTGGCTCTG
 910 920 930 940 950 960
 New 95-04-12- 17.Seq(1>461) <- TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCAGCTA
 New 95-03-30- 09.Seq(1>445) -> TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCAGCTA
 New 95-04-12- 03.Seq(1>447) -> CCCAGCTA
 TGGGCTCCATGTAGAAGCCACTATTACTGGGACTGTGCTCAGAGACCCCTCTCCAGCTA
 970 980 990 1000 1010 1020
 New 95-04-12- 17.Seq(1>461) <- TTCCCTACTCTCTCCCGACTCCGAGAGCATGCTTAATCTGCTTCTGCTTCTCATTTCCTG
 New 95-03-30- 09.Seq(1>445) -> TTCCCTACTCTCTCCCGACTCCGAGAGCATGCTTAATCTGCTTCTGCTTCTCATTTCCTG
 New 95-04-12- 03.Seq(1>447) -> TTCCCTACTCTCTCCCGACTCCGAGAGCATGCTTAATCTGCTTCTGCTTCTCATTTCCTG
 TTCCCTACTCTCTCCCGACTCCGAGAGCATGCTTAATCTGCTTCTGCTTCTCATTTCCTG

1030 1040 1050 1060 1070 1080

New 95-04-12- 17. Seq(1>461) <- TAGCCTGATCAGCGCCGCACCAGCCGGAAAGAGGGTGATTGCTGGGCTCGTG
New 95-03-30- 09. Seq(1>445) -> TAGNCTGATCAGNGCCGCACCAGCCGGAAAGAGGGTGATTGCTGGGCTCGTG
New 95-04-12- 03. Seq(1>447) -> TAGCCTGATCAGCGCCGCACCAGCCGGAAAGAGGGTGATTGCTGGGCTCGTG
New 95-04-12- 11. Seq(1>463) <- AG-TCGTGCCCTGCA
New 95-04-12- 07. Seq(1>453) -> TGGCCCTGCA

TAGCCTGATCAGCGCCGCACCAGCCGGAAAGAGGGTGATTGCTGGGCTCGTG
1090 1100 1110 1120 1130 1140

New 95-03-30- 09. Seq(1>445) -> TCCCTCTCC-TCCCAGGGCTGNCCAC-AGNTC-GGGCCCT-CTGTGAGATCCG-CTT
New 95-04-12- 03. Seq(1>447) -> TCCCTCTCC-TCCCAGGGCTGCCAC-AGCTC-GGGCCCT-CTGTGAGATCCG-CTT
New 95-04-12- 11. Seq(1>463) <- TCCCTCTCCCTCCCAGGCCCTTCCCACAAGCTGGGGCCT-CTGTGAGACCCGT-CTT
New 95-04-12- 07. Seq(1>453) -> TCCCTCTCC-TCCCAGGGCTGCCAC-AGCTC-GGGCCCT-CTGTGAGATCCG-CTT
New 95-04-12- 05. Seq(1>475) -> CGACGGNCAGTGCCAAGCTTGCA

TCCCTCTCC-TCCCAGGGCTGCCAC-AGCTC-GGGCCCT-CTGTGAGAHCCGT-CTT
1150 1160 1170 1180 1190 1200

New 95-03-30- 09. Seq(1>445) -> TNGG-CTCCTCCAGAATGG-GNTGCC-CTCCTGGGATGTGTAATGGTCCCCC-TGCT
New 95-04-12- 03. Seq(1>447) -> T-GGCCTCCCTCCAGAATGGAGCTGCCCTCTCTGGGATGTGTAATGGTCCCCC-TGCT
New 95-04-12- 11. Seq(1>463) <- T-GCCCTCCCTCCAGAATGGAGCTGCCCTCTCTGGGATGTGTAATGGTCCCCCTGCT
New 95-04-12- 07. Seq(1>453) -> T-GGCCTCCCTCCAGAATGGAGCTGCCCTCTCTGGGATGTGTAATGGTCCCCC-TGCT
New 95-04-12- 05. Seq(1>475) -> T-GGCCTCCCTCCAGAATGGAGCTGCCCTCTCTGGGATGTGTAATGGTCCCCC-TGCT

T-GGCCTCCCTCCAGAATGGAGCTGCCCTCTCTGGGATGTGTAATGGTCCCCC-TGCT
1210 1220 1230 1240 1250 1260

New 95-03-30- 09. Seq(1>445) -> TAG
New 95-04-12- 03. Seq(1>447) -> TACCCGC-AAAAGACAAGTCTTACAGAATCAAATGCAATTAAATCTGAGAGCTCGCT
New 95-04-12- 11. Seq(1>463) <- TACCCCCAAAAGACAAGTCTTACAGAATCAAATGCAATTAAATCTGAGAGCTCGCT
New 95-04-12- 07. Seq(1>453) -> TACCCGC-AAAAGACAAGTCTTACAGAATCAAATGCAATTAAATCTGAGAGCTCGCT
New 95-04-12- 05. Seq(1>475) -> TACCCGC-AAAAGACAAGTCTTACAGAATCAAATGCAATTAAATCTGAGAGCTCGCT

TACCCGC-AAAAGACAAGTCTTACAGAATCAAATGCAATTAAATCTGAGAGCTCGCT
1270 1280 1290 1300 1310 1320

New 95-04-12- 03. Seq(1>447) -> TTGAGTGACTGGTTGGTATTGNCTCTGAAGCCTATGTATGCCATGGAGGACTAAC
New 95-04-12- 11. Seq(1>463) <- TTGAGTGACTGGTTTG-TGATTGCCCTCTGAAGCCTATGTATGCCATGGAGGACTAAC
New 95-04-12- 07. Seq(1>453) -> TTGAGTGACTGGTTTG-TGATTGCCCTCTGAAGCCTATGTATGCCATGGAGGACTAAC
New 95-04-12- 05. Seq(1>475) -> TTGAGTGACTGGTTTG-TGATTGCCCTCTGAAGCCTATGTATGCCATGGAGGACTAAC

TTGAGTGACTGGTTTG-TGATTGCCCTCTGAAGCCTATGTATGCCATGGAGGACTAAC
1330 1340 1350 1360 1370 1380

New 95-04-12- 03. Seq(1>447) -> AAACCTCTGAGGTTCCGAAATCAGAAGCGAAAAA-TCAGTGAATAAACCATCATCTTGGC
New 95-04-12- 11. Seq(1>463) <- AAACCTCTGAGGTTCCGAAATCAGAAGCGAAAAAATCAGTGAATAAACCATCATCTTGGC
New 95-04-12- 07. Seq(1>453) -> AAACCTCTGAGGTTCCGAAATCAGAAGCGAAAAAATCAGTGAATAAACCATCATCTTGGNC
New 95-04-12- 05. Seq(1>475) -> AAACCTCTGAGGTTCCGAAATCAGAAGCGAAAAAATCAGTGAATAAACCATCATCTTGGC
AAACCTCTGAGGTTCCGAAATCAGAAGCGAAAAAATCAGTGAATAAACCATCATCTTGGC
1390 1400 1410 1420 1430 1440

New 95-04-12- 03. Seq(1>447) -> ACTA-CCCCTCTGAAGC-ACAGNAGGGT
New 95-04-12- 11. Seq(1>463) <- ACTACCCCTCTGAAGCCACAGCAGGTTCAATC-AGAACTGTTGGC-AAG
New 95-04-12- 07. Seq(1>453) -> ACTACCCCTCTGAAGCCACAGCAGGTTCAATC-AGAACTGTTGG-CAAG
New 95-04-12- 05. Seq(1>475) -> ACTACCCCTCTGAAGCCACAGCAGGTTCAATC-AGAACTGTTGG-CAAG
New 95-03-30- 03. Seq(1>376) <- CNA-NNAGAACTGTTGCCG-G
New 95-03-30- 30. Seq(1>377) <- GATCAAGGGCTTGGCCGAG
New 95-04-12- 09. Seq(1>381) -> CTGTTGGCA-AG

ACTACCCCTCTGAAGCCACAGCAGGTTCAATC-AGAACTGTTGGC-CRAG
1450 1460 1470 1480 1490 1500

New 95-04-12- 11. Seq(1>463) <- GT-GACATTTCCATGCATAATGCGATCCACAGAAGGTCTGGT-GGTATTT-GTAACCT
New 95-04-12- 07. Seq(1>453) -> GT-GACATTTCCATGCATAATGCGATCCACAGAAGGTCTGGTGGTATTTGGTAACCT
New 95-04-12- 05. Seq(1>475) -> GT-GACATTTCCATGCATAATGCGATCCACAGAAGGTCTGGTGGTATTTGGTAACCT
GT-GACATTTCCATGCATAATGCGAWCCACAGRRGGKCTGGKgGGTAtTTgTAACYT

1450 1460 1470 1480 1490 1500

New 95-03-30- 03.Seq(1>376) <- GT-GACATTCCATNCATAAATGCGAACCAAGCAGNNNNCC-NGGNGGNA-TT-TNTACCT
New 95-03-30- 30.Seq(1>377) <- GTGGNAATTCCATNCANAAATGCGAACCCAGGGGGGGGGGGNA-TT-GTAACCT
New 95-04-12- 09.Seq(1>381) -> GT-GACATTCCATGCATAAATGCGATCCACAGAAGGTCTGGT-GGTATTT-GTAACCT
GT-GACATTCCATGCATAAATGCGAWCCACAGRRGGKCTGGKgGGTAtTTgGTAACYI

1510 1520 1530 1540 1550 1560

New 95-04-12- 11.Seq(1>463) <- TTGCAAGGCATTTTTTATATATAT-TTTGTGGCA
New 95-04-12- 07.Seq(1>453) -> TTNGGAAGGNATTTNNNNATATATAT-TTTNGGGAN
New 95-04-12- 05.Seq(1>475) -> TTGGNAAGGC-A-TTNNNNNATATATATTTNGGGCACATTTTTTACGTTCTTT
New 95-03-30- 03.Seq(1>376) <- TTNCAGGCAN-TTTTTAAAAAAANTTGT-NCANATTTTTNTACGNTTCNTNA
New 95-03-30- 30.Seq(1>377) <- TTTCAGGNAATTTTTAAAAAA-NTTGT-GCACANTTTTNCGNNTTCNTNA
New 95-04-12- 09.Seq(1>381) -> TTGNAAGGCATTTTTTATATATAT-TTTGNG-CACATTTTTACGTTCTTTA
TTKSMAGGCATTTTTAWAWAWaTTTGKgRSAMATTTTTACGTTCTTTA

1570 1580 1590 1600 1610 1620

New 95-04-12- 05.Seq(1>475) -> AGAAACAAATGT-TTCAAAATNT-TTAT-GGTCGACAATCAAT
New 95-03-30- 03.Seq(1>376) <- GNAANCCAATGATTCCCCAANATATTANANGCGGACAANTC--ANATANTGGAGTGG
New 95-03-30- 30.Seq(1>377) <- CGANGCCNATNNATNCCCCCANATGTTTATAGGCGNAAAAAA--AAAAATTGGGGNGG
New 95-04-12- 09.Seq(1>381) -> GAAAACAAATGTATTCAAAATATATTATAGTCGAACAATTCAAT-ATATTGAGTGG
GRAARCMATGTATTYCMMATATRTTATAGGCRACAWHMataaAWATTGRRGTGG

1630 1640 1650 1660 1670 1680

New 95-03-30- 03.Seq(1>376) <- ANCCAAATGGATNTCAGTAGTTAACNTCTANTATCCCCAACNGCTGGCCANTNTI
New 95-03-30- 30.Seq(1>377) <- NGCCAANTGGATTTCAGGAGNTNAAACCTCNCNANTATCCCNCCNTGGCCATTNTI
New 95-04-12- 09.Seq(1>381) -> AGCCATATGAATGTCAGTAGTTATACCTCTATTATCTAAACTACTGGCAATTGTA
AGCCAWATGRATKTCAGKAGTTAWACYTCTCTAXTATCYCMAACYRCTGGCMATTIKTW

1690 1700 1710 1720 1730 1740

New 95-03-30- 03.Seq(1>376) <- NAGNAANAAAATGAAAAAANGAATNTGGTTCAGCCTTCATNTAACCNAGTNGATT
New 95-03-30- 30.Seq(1>377) <- AAGGNAAAAAATGAAAAAANGAATNTGGTTCAGCCTTCATNTAACCNAGTNNAAAT
New 95-04-12- 09.Seq(1>381) -> AAGAAATATATATGATATATAAATGTGATTGAGCTTTCAATGTTAGCCACAGTGTATT
AAGRAAWAWAWATGAWAWAXRRATXTGRTTKCAGCYTTCMATXTTARCCXAGTXKAWI

1750 1760 1770 1780 1790 1800

New 95-03-30- 03.Seq(1>376) <- TTTCACTTNTNCCAAAATTNTACCCNATNTNACANTAAATNCCCTANCNAANAAATTNC
New 95-03-30- 30.Seq(1>377) <- TTTCNCTNNNCCNAAATTNNNCCCCATNTNGCNTTAAATTCCNANCCAAANAAATNCN
New 95-04-12- 09.Seq(1>381) -> TTTCACTTGTACTAAAATTGTATCAAATGTGACATTATGCACTAGCAATAAAATGCT
TTTCACTTXXCYAAAATTXTAYCMMATXTXRCATTAWATKCMCTAXCMAWAAAATKCX

1810

New 95-03-30- 03.Seq(1>376) <- GATT
New 95-03-30- 30.Seq(1>377) <- NA
New 95-04-12- 09.Seq(1>381) -> AATGTTTCATGGGTAA
RATGTTTCATGGGTAA